Applied Genome Research

General Introduction

205048 & 205049

Boas Pucker

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2009-2010: Biochemistry

2010-2013: Biology (Genetics, Cell Biology & Physiology)
Functional Genomics, Metabolic Engineering, Comparative Genomics

2013-2015: Genome-based Systems Biology
Synthetic Biology (iGEM2014), Software Development, Genomics

Since 2016: PhD student in Genome Research & Bioinformatics
Plant Genomics, Bioinformatics, Synthetic Biology (iGEM2016/2017/2018)

2018: Visiting Scientist at Brockington Lab, Plant Sciences, University of Cambridge
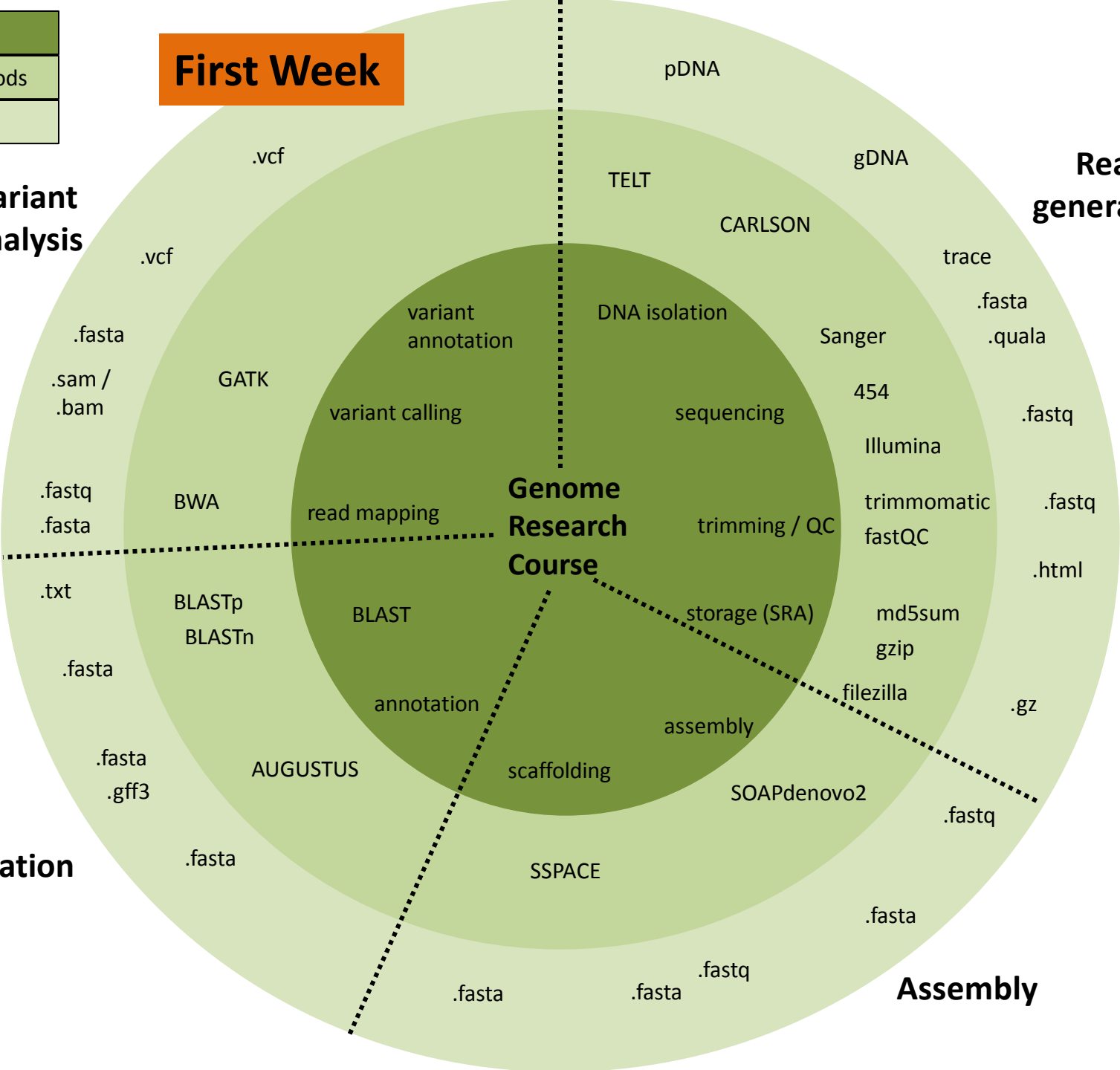
Legend:
- Topic
- Tools / methods
- File formats

Second Week

Genome Research Course

presentation & discussion

experiment design

protocols

data integration & journal club

RNA isolation

analysis

sequencing

Illumina

DeSeq2

Trimming / QC

trimmomatic

featureCounts

Read counting

fastQC

Read mapping

storage (SRA)

md5sum

STAR

gzip

filezilla

File formats:
.pdf
.html
.txt
.txt
.bam
.gff3
.fastq
.fasta
.fastq
.fastq
.html
.fastq
.gz
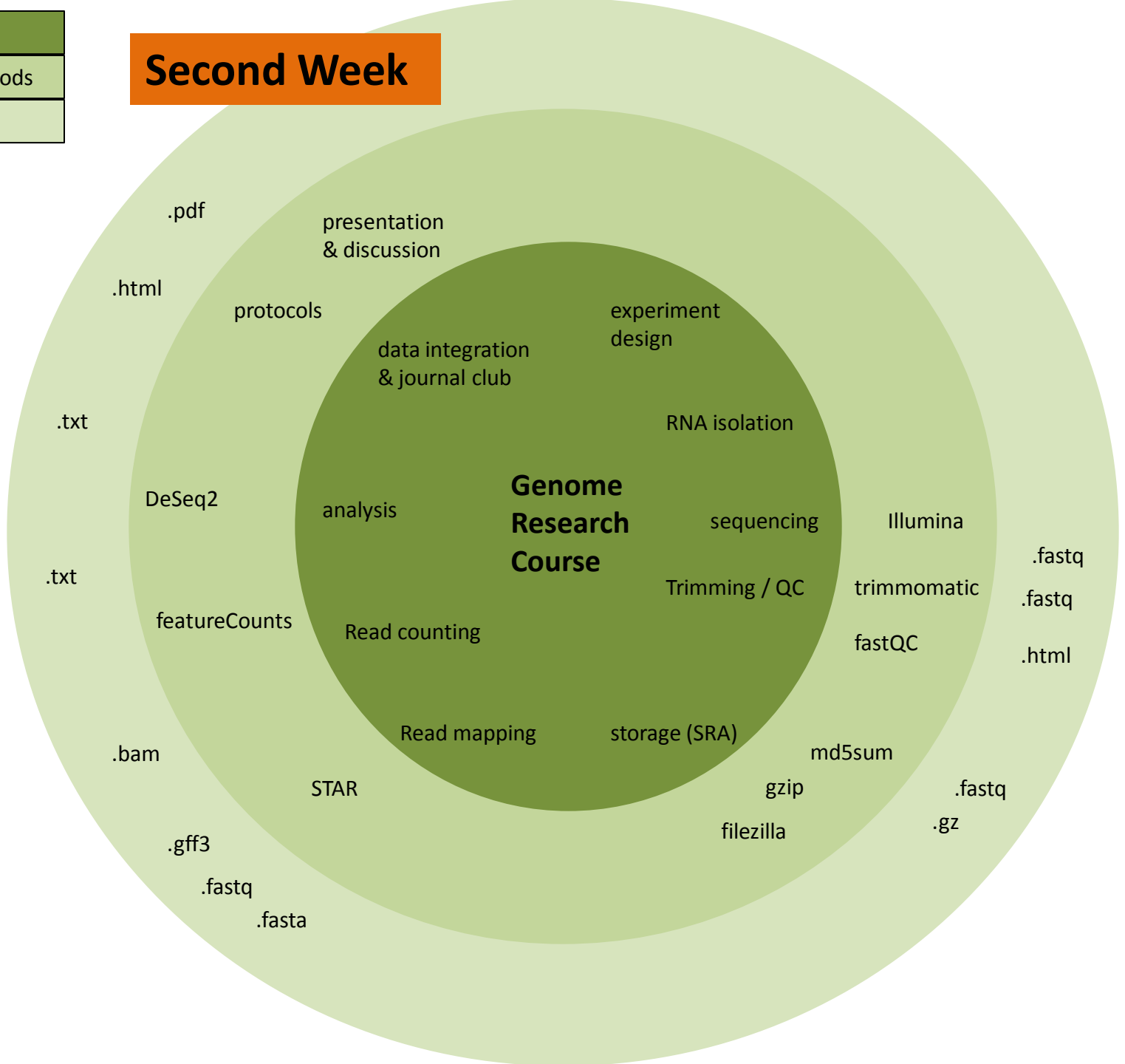
Publications for Journal Club

1. Wendel et al., 2016: Evolution of plant genome architecture.
2. Pucker et al., 2016: A *de novo* genome sequence assembly of the *Arabidopsis thaliana* accession Niederzenz-1 displays presence/absence variation and strong synteny
3. Zapata et al., 2016: Chromosome-level assembly of *Arabidopsis thaliana* Ler reveals the extent of translocation and inversion polymorphisms
4. Xu et al., 2015: De novo assembly and transcriptome analysis of two contrary tillering mutants to learn the mechanisms of tillers outgrowth in switchgrass (Panicum virgatum L.)
5. Olson et al., 2015: Best practices for evaluating single nucleotide variant calling methods for microbial genomics.
6. Alkodsi et al., 2015: Comparative analysis of methods for identifying somatic copy number alterations from deep sequencing data.
7. Huo et al., 2016: Rapid identification of lettuce seed germination mutants by bulked segregant analysis and whole genome sequencing.
8. Zhao et al., 2016: Construction of high-density genetic linkage map and identification of flowering-time QTLs in orchardgrass using SSRs and SLAF-seq.
9. Alkodsi et al., 2015: Comparative analysis of methods for identifying somatic copy number alterations from deep sequencing data
10. Li et al., 2017: Transcriptome analysis reveals differential gene expression and a possible role of gibberellins in a shade-tolerant mutant of perennial ryegrass
11. Mascher et al.., 2017: A chromosome conformation capture ordered sequence of the barley genome
12. Novikova et al., 2016: Sequencing of the genus Arabidopsis identifies a complex history of nonbifurcating speciation and abundant trans-specific polymorphism
13. Leegwater et al., 2016: Dwarfism with joint laxity in Friesian horses is associated with a splice site mutation in B4GALT7
14. Golicz et al., 2016: The pangenome of an agronomically important crop plant Brassica oleracea
15. Tsai et al., 2016: Assembling the Setaria italica L. Beauv. Genome into nine chromosomes and insights into regions affecting growth and drought tolerance
16. Xu et al., 2017: Draft genome of spinach and transcriptome diversity of 120 Spinacia accessions

Data

- Work is based on *Arabidopsis thaliana* Columbia-0 and Niederzenz-1 (Nd-1)
- Sequencing reads are publicly available (in principle)
- Subsets of complete data sets will be used to reduce computation time

- References:
  - TAIR10 (Col-0): https://www.arabidopsis.org
  - Araport11 (Col-0): https://doi.org/10.1111/tpj.13415
  - Nd-1:
    - NGS assembly: https://doi.org/10.1371/journal.pone.0164321
    - Improved annotation: https://doi.org/10.1186/s13104-017-2985-y
    - PacBio assembly: https://doi.org/10.1101/407627